Office

us-09-674-593-1-inv.res

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> O <
O|IO  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-674-593-1-inv.res made by sdavid on Mon 9 Sep 102 12:09:11 PDT.

Query sequence being compared:US-09-674-593-1' (1-1382)
Number of sequences searched:                              8
Number of scores above cutoff:                             8

Results of the initial comparison of US-09-674-593-1' (1-1382) with:
      File : US09674593.seq
```

```
100-

       N
 50-   U
       M
       B
       E

 10-   O
       F

  5-   S
       E
       Q
       U
       E    *
       N  *
       C  *
  0-   S *

SCORE-0     76   152   229   305   381   457   534   610   686
STDEV                    1           1           2
```

```
                    PARAMETERS

Similarity matrix   Unitary
Mismatch penalty          1
Gap penalty            1.00
Gap size penalty       0.33
Cutoff score              0
Randomization group       0

                SEARCH STATISTICS

                Mean     Median    Standard Deviation
                111        26       233.05

Times:          CPU                 Total Elapsed
          00:00:00.00               00:00:00.00

Number of residues:                4494
Number of sequences searched:         8
Number of scores above cutoff:        8

The scores below are sorted by initial score.
Significance is calculated based on initial score.
A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

```
                                                                           Init.  Opt.
Sequence Name    Description                                       Length  Score  Score  Sig.  Frame
-----------------------------------------------------------------------------------------------------
                 **** 2 standard deviations above mean ****                              2.47   0
                 ****   0 standard deviation from mean ****

 1. US-09-674-593-4 Sequence 4, Application US              2167    686    818    2.47   0

 2. US-09-674-593-1 Sequence 1, Application US              1382    222    818   -0.23   0
 3. US-09-674-593-10 Sequence 10, Application US             246     58    222   -0.24   0
 4. US-09-674-593-11 Sequence 11, Application US             613     54    107   -0.34   0
 5. US-09-674-593-9 Sequence 9, Application US                25     32    231   -0.37   0
 6. US-09-674-593-6 Sequence 6, Application US                25     25     25   -0.40   0
 7. US-09-674-593-8 Sequence 8, Application US                18     18     18   -0.40   0
 8. US-09-674-593-7 Sequence 7, Application US                25      9     14   -0.44   0
                                                             18      7     10   -0.45   0
```

```
1. US-09-674-593-1' (1-1382)
US-09-674-593-4 Sequence 4, Application US/09674593

Sequence 4, Application US/09674593
GENERAL INFORMATION:
APPLICANT: Van den Eynde, Benoit
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: TUMOR ASSOCIATED ANTIGEN ENCODED BY THE REVERSE STRAND
TITLE OF INVENTION: OF A NEW UBIQUITOUSLY EXPRESSED GENE
FILE REFERENCE: L0461/7099
CURRENT APPLICATION NUMBER: US/09/674,593
CURRENT FILING DATE: 2000-06-07
PRIOR APPLICATION NUMBER: PCT/US99/10424
PRIOR FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: US 60/085,318
PRIOR FILING DATE: 1998-05-13
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Window Version 3.0
SEQ ID NO 4
LENGTH: 2167
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 303..1730
```

```
Initial Score        =    686   Optimized Score       =   818   Significance  =   2.47
Residue Identity     =    73%   Matches               =   882   Mismatches    =    228
Gaps                 =    95    Conservative Substitutions                                 0
```

```
              10        20        30        40        50        60        70
      CCAGGAACTTAATTGCTTTAATTTGGGAGGAAGCAGGAGGATTGAGGGTAAAGGTGCCAAGAAGAAGAGAGAAAG
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
              80        90       100       110       120       130       140
      AAAAATTAGGCTGTGTTGGAAAGGGTAGCACAGATATGATGTAAGAAATTGGGTTCACCATATTTGTGTGTG
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
             150       160       170       180       190       200       210
      TGTGTGTGGTGCGTCCTCCTCTCCTCCCTCCCTCACTAGGCGTGCCTGTTGTTTGAAGGCCCGCGGCGGTTCCGG
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
             220       230  X     240       250       260       270       280
      CTCCTGCTCCGAAGCCTGCTCCACCTTGATTCTGCCCGTAGCAGGTGAACCTGGTGGTGCGGCCACTGCGGG
         ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
      GTCCACCTTGATTCTGCCCGTAGCAGGTGAACCTGGTGGTGCGGCCACTGCGGG
       X       10        20        30        40        50
```

```
             290       300       310       320       330       340       350       360
      TCCTGATTGGCTGTGCACGGCCACGGTGAAAAACTTGAGCGTCTACTACTCCGAGTCCTGCAAGCTCCTAGTGTCT
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      TCCTGATTGGCTGTGCACGGCCACGGTGAAAAACTTGAGCGTCTACTACTCCGAGTCCTGCAAGCTCCTAGTGTCT
              60        70        80        90       100       110       120
```

```
             370       380       390       400       410       420       430
      CCTCTGGGTGGACGCGCTAGGCGCACGGCCGTTACTTCTTCTTTCACCTGTGGATTCGTCAGTTTCGTCGTTCGT
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      CCTCTGGGTGGACGCGCTAGGCGCACGGCCGTTACTTCTTCTTTCACCTGTGGATTCGTCAGTTTCGTCGTTCGT
             130       140       150       160       170       180       190       200
             440       450       460       470       480       490       500
```

```
        840       850       860       870       880       890       900
GCTGCGCGCTCATCTTCCCCGCTGCCGCCGCCTCAGCTCGCTCGCTTCGCGTCGGAGGCACCTCCGCTGTCC

        910       920       930       940       950       960       970   980
CAGCGGCCTCACCGCACCCAGGGCGCGGGATCGCCTCCTGAAACGAGCGAGAAACTGACGAATCCACCAGGTG

AAAGAGA
```

3. US-09-674-593-1' (1-1382)
   US-09-674-593-10 Sequence 10, Application US/09674593

Sequence 10, Application US/09674593
GENERAL INFORMATION:
 APPLICANT: Van den Eynde, Benoit
 APPLICANT: Boon-Falleur, Thierry
 TITLE OF INVENTION: TUMOR ASSOCIATED ANTIGEN ENCODED BY THE REVERSE STRAND
 TITLE OF INVENTION: OF A NEW UBIQUITOUSLY EXPRESSED GENE
 FILE REFERENCE: L0461/7099
 CURRENT APPLICATION NUMBER: US/09/674,593
 CURRENT FILING DATE: 2000-06-07
 PRIOR APPLICATION NUMBER: PCT/US99/10424
 PRIOR FILING DATE: 1999-05-13
 PRIOR APPLICATION NUMBER: US 60/085,318
 PRIOR FILING DATE: 1998-05-13
 NUMBER OF SEQ ID NOS: 11
 SOFTWARE: FastSEQ for Window Version 3.0
 SEQ ID NO 10
 LENGTH: 246
 TYPE: DNA
 ORGANISM: Homo sapiens

Initial Score   =   54   Optimized Score   = 107   Significance = -0.24
Residue Identity = 51% Matches   = 137   Mismatches   =   85
Gaps   =   44   Conservative Substitutions = 0

```
[DNA sequence alignment data - reverse strand comparison, positions 650-1270 and 10-130]
```

Right column

```
      220       230       240       250       260       270       280
CTCCCTGCTCAGAAGCTGTCCACCTTGATTCTGCCCGTAGCAGTGAACCTGGTGTCGTGGTGCGGCCACTGCGGG
      290       300       310       320       330       340       350       360
TCCTGATTGGCTGCTGCACGCCACGCGCTCACTCCGAGTCGTCTACTTCTTTCACCTGTGGATTCGTCAGTTTCGTTCGT
                 370       380       390       400       410       420       430
CCTGGTGGACGCCTAGGGCGACACGCCGGCCGTACTTCTCTTTCACCTGTGGACGCGGGGTGCTCCCGACGCGGGAAGC
          440       450       460       470       480       490       500
TTCAGGAGGGGATCCCGCCGGTGGTGCGGTGGACGCGGGAGGCGAGGAAGCGAGGAAGC
          510       520       530       540       550       560       570
AGCGAGCTGAGGCGGCGGGCCAGCGGGGAAGATGAGCGCAGCGGCCAGGTCCAGCCACCTGTCTCAGCCC
      580       590       600
GTCGTGAAGAGCGTGCTTGTGTACCGC
```

```
6. US-09-674-593-1' (1-1382)
   US-09-674-593-6 Sequence 6, Application US/09674593

Sequence 6, Application US/09674593
GENERAL INFORMATION:
  APPLICANT: Van den Eynde, Benoit
  APPLICANT: Boon-Falleur, Thierry
  TITLE OF INVENTION: TUMOR ASSOCIATED ANTIGEN ENCODED BY THE REVERSE STRAND
  TITLE OF INVENTION: OF A NEW UBIQUITOUSLY EXPRESSED GENE
  FILE REFERENCE: L0461/7099
  CURRENT APPLICATION NUMBER: US/09/674,593
  CURRENT FILING DATE: 2000-06-07
  PRIOR APPLICATION NUMBER: PCT/US99/10424
  PRIOR FILING DATE: 1999-05-13
  PRIOR APPLICATION NUMBER: US 60/085,318
  PRIOR FILING DATE: 1998-05-13
  NUMBER OF SEQ ID NOS: 11
  SOFTWARE: FastSEQ for Window Version 3.0
SEQ ID NO: 6
  LENGTH: 18
  TYPE: DNA
  ORGANISM: Homo sapiens

Initial Score  = 18    Optimized Score = 18    Significance = -0.40
Residue Identity = 100%  Matches = 18    Mismatches = 0
Gaps = 0                 Conservative Substitutions = 0
```

```
      220       230       240       250       260       270       280
GCTCCGTCCAGAAGCTGTCCACCTTGATTCTGCCCGTAGCAGTGAACCTGGTGTCGTGGTGCGGCCACTGCGG
      290       300       310       320       330       340       350
GTCCTGATTGGCTGCTGCACGCCACGCGCTCACTCCGAGTCGTCTACTTCTTTCACCTGTGGATTCGTCAGTTTCGTTCG
      360       370       380       390       400       410       420       430
TCCTCTGGGTGGACGCCTAGGGCGACGGCACGCCGGCCGTACTTCTCTTTCACCTGTGGATTCGTCAGTTTCGTTCGTCG
      440       450       460       470       480       490       500
TTTCAGGAGGGGATCCCGCCGGTGGTGCGGTGGACGCGGGAGCAGCGGAGGTGCTCCCGACGCGGAAG
      510       520       530       540       550       560       570
CAGCGAGCTGAGGCGGCGGGCCAGCGGGGAAGATGAGCGCAGCGGCCAGTTCCAGCCACCTGTCTCAGCC
      580       590       600       610       620       630       640
CGTCGTGAAGAGCGTGCTTGTGTACCGCCAACGGGGCCCCCGTCTCATCCATGA
      650       660       670       680       690       700       710
GAAGAAGGTGTCAGCTTCAGTCTCCTGAAGGAGTGACCGGCGCGGTTCAGGCACCCTTGGGCCGT
      720       730 x   740       750       760       770       780       790
CAGGAACATCTACACCCCGGCGACTGGCCACCGAATCCGGAGCTAGACCAGATCCAGAGCGGGGCAATTA
      |||||||||||||||||
```

Left column

```
      900       910       920       930       940       950       960
TGCA--GATCCCTACCCCCACCACTCAGTGGTTGAGGGCGTGACCTTCCGGTGATGATGATGCCCCTC
      ||||-|-||||  ||  ||||-|-||  |||-|-||-||-||||  |-||||  |-||||-|-||
TGCATNGCTTNGTTGGCTCCCAATGNGCCGCACGCTCA--GGAAGAAGTTGTTNAAGGGA--GNACCCNGTT
      420       430       440       450       460       470       480
      970       980       990      1000      1010      1020      1030
AAAACTCTCGTTGCAGTTGGGGGGTGAGAGTTGACACTGTGACTGGAGAGGAATTTCACTTGG-GTCAGCA
      |-||  |-|||-||-||||  |||| -|-||||  |  |||| -|-|||-|-||||  |||
ANAGTTTATAAAGC--CTGGATGGTA-TGGTTNGCCGAGT-AATG-----NGAAATCCTGTGGGANTTTCCA
      490       500       510       520       530       540
     1040      1050      1060      1070      1080      1090      1100
GTAGGAGTAAACTAAAATCTGTGTATAAAACAGGAATCTAAAGAAAATAAAAAAGGTATCCTGCAAAG
      |  |-||||  ||||   ||||   ||||  ||   |-|||-|||   |||  |||-||
CT--GA-TCCAGGTCCAATC----TTTACCCAGTAGNTATC------TCTCTCCNTCTCC---CTTAT
550                560               570       580       590       600
     1110      1120      1130      1140      1150      1160      1170
GTTAGTGACCAAACTGATACTTTTGCGTTTTCGTTCGTTTCAGTTTTTTCCTTTTTCCTTTTATTTTTTTTCCTT
      ||||-||-|||
GTTATTGGGAA
       610 x
```

```
     1180      1190      1200      1210      1220      1230      1240      1250
GGAAATCCATCCTTTTAATTTAAATAAACATTCTTAAAAATCACTTCCAAGTGTTGGACACTATATTGCCAC
     1260      1270      1280      1290      1300      1310      1320
CAGAGGAGAAAATTGCTCTGCATTTCCCGTACTGTTTAAATTAATTTCAACCTTTCATTCCAAGTAGAATTGA
     1330      1340      1350      1360      1370      1380
CAACACTCACTTTTGTGACCCTGCTCCCACCCCCTGCCATGTTTATGCTGTTAGCATAAATG
```

```
5. US-09-674-593-1' (1-1382)
   US-09-674-593-9 Sequence 9, Application US/09674593

Sequence 9, Application US/09674593
GENERAL INFORMATION:
  APPLICANT: Van den Eynde, Benoit
  APPLICANT: Boon-Falleur, Thierry
  TITLE OF INVENTION: TUMOR ASSOCIATED ANTIGEN ENCODED BY THE REVERSE STRAND
  TITLE OF INVENTION: OF A NEW UBIQUITOUSLY EXPRESSED GENE
  FILE REFERENCE: L0461/7099
  CURRENT APPLICATION NUMBER: US/09/674,593
  CURRENT FILING DATE: 2000-06-07
  PRIOR APPLICATION NUMBER: PCT/US99/10424
  PRIOR FILING DATE: 1999-05-13
  PRIOR APPLICATION NUMBER: US 60/085,318
  PRIOR FILING DATE: 1998-05-13
  NUMBER OF SEQ ID NOS: 11
  SOFTWARE: FastSEQ for Window Version 3.0
SEQ ID NO 9
  LENGTH: 25
  TYPE: DNA
  ORGANISM: Homo sapiens

Initial Score  = 25    Optimized Score = 25    Significance = -0.37
Residue Identity = 100%  Matches = 25    Mismatches = 0
Gaps = 0                 Conservative Substitutions = 0
```

```
       10        20        30        40        50        60        70
CCAGGAACTTAATTGCTTTAATTGGGAGGAAGCCAGGAGATTGAGGGGTAAAGGTGCAAGAAGAGAGAAAAG
        80        90       100 x     110       120       130       140
AAAAATTAGGCTGTGTTGAAAAGGGTAGCACAGATATGATGTAAGAAAATTGGGTTTCACCATATTGTGTGTG
      |||||||||||||||||||||                                          |||-|
TAGGCTGTTTGGGAAAGGGTAGCACA                                        CCGT
       10        20 x                                                  x
      150       160       170       180       190       200       210
TGTGTGTGTGTGCGGTCCCTCTCGCTCCTCTCGCTCCTCACTCAGCGTGCCCTGTTTGAAGGGCCCCGCGTTCCGG
```

```
                                                       CCA-
                                                       X
        560       570       580       590       600       610       620
GTCCAGCCACCTGTCTCAGCCCGTCGTGAAGAGCCGTGCTTGTGTACCGCAACGGGGACCCCTTCTACGCGGG
         |||||||  |  |
        --ACAGCCACATAAAAC
                10   X

        630       640       650       660       670       680       690
GCGCCGCGTCGTCATCCATGAGAGAAGGTGTCCAGCTTGCGAAGTCTTCCTGAAGGAGGTGACCGCGGCGT

700       710       720       730       740       750       760       770
TCAGGCACCCTTTGGGCCCGTCAGGAACATCTACACCCCGCGACTGCCACCGAATCCGGAAGCTAGACCA

        780       790       800       810       820       830       840
GATCCAGAGCGGGGGCAATTACGTGGCTGGAGGCCAGGAAGCCTTCAAGAAACTCAAGTGAGTCGGTCTCCC

        850       860       870       880       890       900       910
CCACCGCCCACCCATTTAGGTGCCCTATAGTGTGGGGTTGATATGAAGAAATGCAGATCCCTACCCCCCAC

        920       930       940       950       960       970       980
ACCTCAGTGGTTGAGGGCGTGTGACTTCTCGGTGATTGATGCCCCTCAAAACTCTCGTTGCAGTTGGGGG

        990      1000      1010      1020      1030      1040      1050
GTAGAGGTTGACACTGTGACTGGAGAGGAATTTCACTTGGGTCAGCAGTAGGAGTAAACTTAAAATCTGTG

1060      1070
TATAAACAACAGG
```

SEQ ID 4

```
              GenCore version 4.5
        Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:        September  6, 2002, 07:29:33 ; Search time 1.42 Seconds
                                              (without alignments)
                                              4.218 Million cell updates/sec

Title:          us-09-674-593-1
Perfect score:  1382
Sequence:       1 cattatgctaacagcataa..........taaagcaattaagttcctgg 1382

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 0.5

Searched:       1 seqs, 2167 residues

Total number of hits satisfying chosen parameters:    2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

st-processing: Minimum Match 0%
               Maximum Match 100%
               Listing first 2 summaries

Database :      us-09-674-593-4:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                        SUMMARIES
              %
Result       Query
NO.   Score  Match Length DB ID                        Description
----  -----  -----  ------ -- --               -----------------
c  1  595.4   43.1   2167  1  us-09-674-593-4    Complement of
   2   30      2.2   2167  1  us-09-674-593-4    Result 4

                        ALIGNMENTS

RESULT   1
us-09-674-593-4/c

Query Match         43.1%;  Score 595.4;  DB 1;  Length 2167;
est Local Similarity  99.8%;  Pred. No. 0;
atches   596;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy  554 acttagtttcttgaaggctccagccttgccccgcctctggatct 613
            | ||||||||||||||||||||||||||||||||||||||||||
Db  597 AATTGAGTTTCTTGAAGGCTTCCTGGCCTCCAGCCACGTAATTGCCCCCGCCTCTGGATCT 538

Qy  614 ggtctagcttccggattcggtggccagtccgcggggtgagatgttcctgacggcccaa 673
            ||||||||||||||||||||||||||||||||||||||||||||||||
Db  537 GGTCTAGCCTTCCGGATTCGGTGGCCAGTCCGCGGGGTGAGATGTTCCTGACGGCCCCAA 478

Qy  674 agggtgcctgaacgccgccggtcacctccttcaggaagacttgaagctggacaccttct 733
            |||||||||||||||||||||||||||||||||||||||||||||
Db  477 AGGGTGCCTGAACGCCGCCGGTCACCTCCTTCAGGAAGACTTCGAAGCTGGACACCTTCT 418

Qy  734 tctcatggtgacgacggccgcggccccggcccccgtagaaggggtccccgttgcggtacacaagca 793
            ||||||||||||||||||||||||||||||||||||||||||||||
Db  417 TCTCATGGATGACGACGGCCGCGGCCCCGGTAGAAGGGGTCCCCGTTGCGGTACACAAGCA 358

Qy  794 cgtcttcacgacgggctgagacagtgctggacctggccgctctgctcgccgcctcatcttcc 853
            ||||||||||||||||||||||||||||||||||||||||||||
```

```
Db  357 CGCTCTTCACGACGGGCTGAGACAGTGGCTGGACCTGGCGCTGCTGCCGCTCATCTTCC 298
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  854 cgcctggccgcgcctcagctcgctcttcgtcggaggcacctcgctcgtcccagcg 913
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  297 CCGCTGGCCGCGCCGCCTCAGCTCGCGCTTCGCCGTCGGCGGAGGCACCTCCGCGTCCCAGCG 238

Qy  914 gcctcaccgcaccaggcgcggatcgccctcctgaaacgaacgagaaactgacgaatcc 973
            |||||||||||||||||||||||||||||||||||||||||||||||||
Db  237 GCCTCACCGCACCCAGGGGCGGGAGATCGGCCTCCTGAAACGAGCGAAACTGACGAATCC 178

Qy  974 acagtgaaagagagtaacggccgtgccgtaggcgtcacccagaggagagacactagga 1033
            |||||||||||||||||||||||||||||||||||||||||||||||||
Db  177 ACAGTGAAAGAGAGTAACGGCCGTGCCGCCTAGGCGTCACCCAGAGGAGACACTAGGA 118

Qy  1034 gcttgcaggactcggatagacgctcaagtttttcaccgtgcgtgcacagccaatcagg 1093
            |||||||||||||||||||||||||||||||||||||||||||||||||
Db  117 GCTTGCAGGACTCGGATAGACGCTCAAGTTTTTCACCGTGCGTGCACAGCCAATCAGG 58

Qy  1094 acccgcagtgcgcgcaccaccaggttcacctgctacgggcagaatcaaggtggac 1150
            |||||||||||||||||||||||||||||||||||||||||||||||
Db   57 ACCCGCAGTGCGCGCCACCACCAGGTTCACCTGCTACGGGCAGAATCAAGGTGGAC 1

RESULT  2
us-09-674-593-4

Query Match          2.2%;  Score 30;  DB 1;  Length 2167;
Best Local Similarity  49.4%;  Pred. No. 0;
Matches   78;  Conservative   0;  Mismatches   80;  Indels   0;  Gaps   0;

Qy  739 tggatgacgacggcgcgccccgcgtagaaggggtcccgttgcggtacacaagcacgctc 798
            || |||||| ||   ||||||||  ||||| || |||||||| || |||||
Db  255 tgcctcccgacgcaagcgagctgagctgagctggggttcgccagcgggagatgagcggcagc 314

Qy  799 ttcacgacgggctgagacagtggctggacctggccgctctgctcgccctcatcttcccccgct 858
            ||| |||||||||||||||||||||||||||  ||| |||||||| ||| ||
Db  315 agccgccagtgccagtccagccgtctcagccgtcgtgaagagcgtcgttgtgtaccgcaac 374

Qy  859 ggccgccgcctcagctcgctcgttcggtcggggaggca 896
            || ||||||| |||||| || || |||||| ||
Db  375 gggaccccttctacgcggggcgccgcgctcgtcatcca 412

Search completed: September  6, 2002, 07:29:36
Job time: 3 sec
```

OM protein - protein search, using sw model

Copyright GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

Run on: September 6, 2002, 07:32:44 ; Search time 0.01 Seconds
                                             (without alignments)
                                             3.998 Million cell updates/sec

Title:
Perfect score: us-09-674-593-2
Sequence: 451
                 1 MDDDAAPRVEGVPVAVHKHA.........GAGSPPETNEKLTNPQVKEK 84

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 476 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

st-processing: Minimum Match 0%
               Maximum Match 100%
               Listing first 2 summaries

Database :   us-09-674-593-5:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                              SUMMARIES

                  %
Result   Query
 NO.. Score Match Length DB ID   Description
 ---- ----- ----- ------ -- --------------------------------
   1   51 11.3   476 1 us-09-674-593-5

                             ALIGNMENTS

RESULT 1
us-09-674-593-5

Query Match   11.3%;   Score 51; DB 1; Length 476;
Best Local Similarity 23.1%;   Pred. No. 0;
 atches   21; Conservative 10; Mismatches 40; Indels 20; Gaps   2;

Qy   4 DAAPRVEGVPVAVHKHALHDGLRQVAGPGAAAAHLPRWPPQLAASRREAPPLSQRPHRT 63
        || ||:|| |:|||| |: | :: :   :: :: ::
Db 383 DAPEQVE-------EILDHSEQQARPARVNGGTDEENGEELQQVNNELQLVLDKERKS 433

Qy   64 QGAGS----------PPETNEKLTNPQVKE 83
        ||||| || |:|:|:| |
Db 434 QGAGSGQDEADVDPQRPRPEVKITSPEENE 464

Search completed: September 6, 2002, 07:32:44
Job time: 0 sec

```
1280      1290       1300       1310       1320       1330
CGTACTG--TTTAAATATTTCAACCTTTCATTC-CAAGTAGAATTGACA-ACACTC----ACT--TTTGTG
| |||  | :|:|| | ||||  ||| | |||  |||| ||| ||| |||            |||   ||||
CCAACTGCAACGAGAGTTTTGAGGGCATCAATCACCAGAGAGTCACAGCCCCTCAACCACTGAGGTGTG
      140      150       160       170       180       190      200

1340      1350       1360       1370       1380 x
ACCCTGCTCCACCCCTGCATGTTTATGCTGTTA---GCATAATG
        ||||||| || |||| ||  | | ||
GGGGGTAGGGA---TCTGCAT-TTCTTCATATCAACCCCACACTA
      210      220      230       240 X
```

4. US-09-674-593-1' (1-1382)
US-09-674-593-11 Sequence 11, Application US/09674593

GENERAL INFORMATION:
    APPLICANT: Van den Eynde, Benoit
    APPLICANT: Boon-Falleur, Thierry
    TITLE OF INVENTION: TUMOR ASSOCIATED ANTIGEN ENCODED BY THE REVERSE STRAND
    TITLE OF INVENTION: OF A NEW UBIQUITOUSLY EXPRESSED GENE
    FILE REFERENCE: L0461/7099
    CURRENT APPLICATION NUMBER: US/09/674,593
    CURRENT FILING DATE: 2000-06-07
    PRIOR APPLICATION NUMBER: PCT/US99/10424
    PRIOR FILING DATE: 1999-05-13
    PRIOR APPLICATION NUMBER: US 60/085,318
    PRIOR FILING DATE: 1998-05-13
    NUMBER OF SEQ ID NOS: 11
    SOFTWARE: FastSEQ for Window Version 3.0

SEQ ID NO 11
    LENGTH: 613
    TYPE: DNA
    ORGANISM: Homo sapiens
    FEATURE:
        NAME/KEY: unsure
        LOCATION: 242..242
        OTHER INFORMATION: n = a, c, g or t
        NAME/KEY: unsure
        LOCATION: 317..317
        OTHER INFORMATION: n = a, c, g or t
        NAME/KEY: unsure
        LOCATION: 320..320
        OTHER INFORMATION: n = a, c, g or t
        NAME/KEY: unsure
        LOCATION: 424..424
        OTHER INFORMATION: n = a, c, g or t
        NAME/KEY: unsure
        LOCATION: 429..429
        OTHER INFORMATION: n = a, c, g or t
        NAME/KEY: unsure
        LOCATION: 444..444
        OTHER INFORMATION: n = a, c, g or t
        NAME/KEY: unsure
        LOCATION: 470..470
        OTHER INFORMATION: n = a, c, g or t
        NAME/KEY: unsure
        LOCATION: 478..478
        OTHER INFORMATION: n = a, c, g or t
        NAME/KEY: unsure
        LOCATION: 483..483
        OTHER INFORMATION: n = a, c, g or t
        NAME/KEY: unsure
        LOCATION: 488..488
        OTHER INFORMATION: n = a, c, g or t
        NAME/KEY: unsure
        LOCATION: 516..516
        OTHER INFORMATION: n = a, c, g or t
        NAME/KEY: unsure
        LOCATION: 528..528
        OTHER INFORMATION: n = a, c, g or t
        NAME/KEY: unsure
        LOCATION: 543..543
        OTHER INFORMATION: n = a, c, g or t
        NAME/KEY: unsure
        LOCATION: 579..579
        OTHER INFORMATION: n = a, c, g or t
        NAME/KEY: unsure
        LOCATION: 591..591
        OTHER INFORMATION: n = a, c, g or t
```
Initial Score        =  231   Significance             = -0.34
Residue Identity     =  44%   Matches = 294  Mismatches =  273
Gaps                 =  98    Conservative Substitutions =    0


CCAGGAACTTAATTGCTTAATTTGGAGGAGCAGGAGATTGAGGGTAAAGGTGCAAGAAGAGAGAAAG
        10        20        30        40        50        60       70

AAAAATTAGGCTGTGTTTGGAAAGGTAGCACAGATATGATGTAAGAAATTGGGTTTCACCATATTTGTGTG
        80        90       100       110       120       130       140

TGTGTGTGTGGCGTCCTCCTCTCTGCCCTCACTAGGCGTGCCTGTTTGAAGGCCCCGGCGTTCCGG
       150       160       170       180       190       200       210

CTCCTCCTCAGAAGCTGTCCACCTTGATTCTGCCCGTAGCAGGTGAACCTGGTGTGTGCGCGCACTGCGGG
       220       230       240       250       260       270       280

TCCTGATTGGCTGTGCACGCCACGGTGAAAACTTGAGCGTCTACTCCGAGTCCTGCAAGCTCCTAGTGTCT
       290       300       310       320       330       340       350    360

CCTCTGGGTGGACGCGTCTAGGGCACGGCCGTTACTTCTCTTTCACCTGTGGATTCGTCAGTTTCTCGTTCGT
       370       380       390       400       410       420       430

TTCAGGAGGCGATCCCGCGCCCTGGGTGCGGTGAGGCGCGTGGGACAGCGGAGGTGCCTCCCGACGCGAAGC
       440       450       460       470       480       490       500
GAAGA
X

A-GCGAGCTG--AGGCGGCGGCCAGGGGGGA-GATGAGCGGCAGCGCCAGGTCCAGCCACCTGTCTCA
       510       520       530       540       550       560       570
| | ||||| |  ||:||| ||  || ||  |||||||| | ||| |||||| |  || ||| |||
ATTTGCACTGGAAGACAATTGCCACTTGTAAAGGATGAAAAAATAGGATC-ACTCTTATTGTACGCTTTATTA
        10        20        30        40        50        60       70

GCCCGTCGTGAAGAGCTGCTTGTGTACCGCAACGGGGACCCCTTCTACGGCGGGCGCCGCGTCGTCATCCA
       580       590       600       610       620       630       640
||| ||| |||  |||||  | ||  ||  |||||| ||||||| ||| ||||| |||||| | |||||
-TAAGTTTAGAAG-GC-AGTTTAT---TCTAAATAATTTTC--TCTA-GGAAGGCGTAGAATTTTAAAGAA
        80        90       100       110       120       130

-TG---AGAAGAAGG--TGT-CCAGCTTC--GAAG-----TCTTCCTGAAGGAGGTGACCGGCG----GCGT
       650       660       670       680       690
|| |   ||||||| |  ||| |||| |   ||||         ||||| ||| | ||| |||     ||||
CTGGTAATAGAAAGCATGTACTATTTTCTTAAAGCAATAAACTCTTGAATGAACAGA-TTGCGATTTACTT
      140       150       160       170       180       190       200    210

TCAGGACACCCTTTGGGCCGTCAG--GAACA-----TCTACA--CCCCGCGGACTGGCC--ACCGAATCCGG
       700       710       720       730       740       750
||| ||||  |||||||| |||||  |||||       || ||  ||| || ||| ||     || ||||||
TCAGACATAATTTGGAGATGGCAGTAGATCANAAATGTGTCCATGACTTGTTAACATGCCTTTCCG-TTCTTC
      220       230       240       250       260       270       280

AAGCT--AGACCAGATCCA--GAGCCGGGGGCAATTACGTGGCTGGAGGCCAGGAAGCCTTCAAGAAACTCAA
       760       770       780       790       800       810       820
|||||  || ||||| | ||  |||| ||| |||||| || || |||| ||  ||| |  || || ||||| ||
CTCCTTAAGCCAAAATCCACCTTTGACTACAAAATNCCNG--AGCAAGGCGTTCATTTTTGGTGGGAAGGAA
      290       300       310       320       330       340       350

GTGAGTCGGTCTCCCCCACCGCGCCACCCATTTAGGTCCCTATAG-TGTGGGGT----TGATATG-AAGAAA
       830       840       850       860       870       880       890
|||| | ||  || |||  | ||||| ||||| |||  |  || ||       |     | |||| ||||||
G-CATTGGGT-TC-AGGAGTG-TTAGTGA-CTAGTATCGCCATTGCCTTAAGTCCGTTTGCAGGCTT
      360       370       380       390       400       410
```

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                                                           |    |||  |  |  ||  |     ||||  ||   |  |||  |||||  |||  ||
                                                  CTATTGTAGGATCCAGAAAGTCTAAAGGGA--GTGAAATGATCGCCA-CTCTAAGTCAACAGTTGGATCCA
                                                  1030      1040      1050      1060      1070      1080      1090

                                                 1320      1330      1340      1350      1360      1370      1380 X
                                                 -TGACAACACTCA-CTTTTGTGACCCTG--CTCCCACCCCTGCATGTTA--TTA--TGCTGTTAGCATAATG
                                                 GTGACA--ACTCATCTCCTCAGCCCCTGAACGGGGAAAAAGAGACGTGAAТTCAGAAAAACTGAC
                                                 1100      1110      1120      1130      1140      1150      1160 X

                                                 GAAATTGAAACAAAATGTAAAATTAAAGAATTCACAAGAAACCATTCCAAATAGTGATGAAGGCATTTCAA
                                                 1170      1180      1190      1200      1210      1220      1230      1240

                                                 AGCTGGACGAGAGGTCTGAAACACGGGGCCAGCAGAGTCCAAGAAGATGAAGAATACTCAGGTTGAGGT
                                                 1250      1260      1270      1280      1290      1300      1310

                                                 TCCAGTTCGATCAGAGGCCAGCAGAAATAGTAGACGAGGAAGAATGGAGAGAAGAACAAGGATGCAGA
                                                 1320      1330      1340      1350      1360      1370      1380

                                                 ACAGAAGAAGGACTTTCAGGAATGAATGGTGACCTTGAAGAGGAAGGAGGTAGGAGGCTACAGATGCCCC
                                                 1390      1400      1410      1420      1430      1440      1450

                                                 TGAGCAAGTCGAGGAGATTCTGGATCACAGTGAGCAGCAGCACGCCCTGCTCGTGTAAATGGAGGCACCGA
                                                 1460      1470      1480      1490      1500      1510      1520

                                                 TGAGGAGAATGGTGAGGAGCTGCAGCAGGTTAATAATGAGCTTCAACTGGTCCTAGACAAGGAAAAGAAAGTC
                                                 1530      1540      1550      1560      1570      1580      1590      1600

                                                 TCAAGGAGCTGCAGTGGACAAGATGAGGCTGATGTGAGTAGACCCTCAAAGACCAAGGCCAGAG
                                                 1610      1620      1630      1640      1650      1660
```

2. US-09-674-593-1' (1-1382)
   US-09-674-593-1 Sequence 1, Application US/09674593

Sequence 1, Application US/09674593
GENERAL INFORMATION:
  APPLICANT: Van den Eynde, Benoit
  APPLICANT: Boon-Falleur, Thierry
  TITLE OF INVENTION: TUMOR ASSOCIATED ANTIGEN ENCODED BY THE REVERSE STRAND
  TITLE OF INVENTION: OF A NEW UBIQUITOUSLY EXPRESSED GENE
  FILE REFERENCE: L0461/7099
  CURRENT APPLICATION NUMBER: US/09/674,593
  CURRENT FILING DATE: 2000-06-07
  PRIOR APPLICATION NUMBER: PCT/US99/10424
  PRIOR FILING DATE: 1999-05-13
  PRIOR APPLICATION NUMBER: US 60/085,318
  PRIOR FILING DATE: 1998-05-13
  NUMBER OF SEQ ID NOS: 11
  SOFTWARE: FastSEQ for Window Version 3.0
  SEQ ID NO 1
    LENGTH: 1382
    TYPE: DNA
    ORGANISM: Homo sapiens
    FEATURE:
    NAME/KEY: CDS
    LOCATION: 738..989

Initial Score =	58
Residue Identity =	51%
Gaps =	64

Optimized Score =	222
Matches =	267
Conservative Substitutions =	64

Significance =	-0.23
Mismatches =	188
=	0

```
                                                 400       410       420       430       440       450       460
                                                 TCTCTTTCACCTGTGGATTCTGTCAGTTTCTCGTTCGTTTCAGGAGGCGATCCGCCGCGCCTGGGTGCCGGTGAG
                                                 GCCGCTGGGACAGCGGACCGGAGGTGCCTCCCGACGCGAAGCCAGCAGCGGAGCTGAGGCGGCCAGCGCGGGAAGATGAG
                                                 470       480       490       500       510       520       530

                                                 540       550       560       570       580       590       600       610
                                                 CGGCAGCGGCCCAGGTCCAGCCACCTGCTCATCCATGAGAAGGTGTCCAGCTTCGAAGTCTTCCTGGAAGGA
                                                 CCCCTTCTACCGCGGGGGCGCCGCGCGTCGTCATCATCATGAGAGAAGGAGGTGTTCCAGTTCCAAGTTCTTCCTGAAGGA
                                                 620       630       640       650       660       670       680
```

CAGGAACACTATACA
10
x

```
        800       810       820       830       840       850       860
CGTGGCTGGAGGCCAGGAAGGCCTTCAAGAAACTCAAGTAGTGAGTCGTCTCCCCACCGGCCCCACCCCATTTAGGT

        870       880       890       900       910       920       930
GCCCTATAGTGTGGGGTTGGGGTTGATTATGAAGAAATGCAGAATCCCTACCCCAGCCCACACCTGGTGTTGAGGGGCTG

        940       950       960       970       980       990      1000
TGACTTCTCCGGTGTGAATTGATGCCCTCAAAAACTCTCGTTGCCAGTTGGGGGGTAGAGGTTGACACTGTGACT

       1010      1020      1030      1040      1050      1060      1070
GGAGAAGGAAATTCACTGGGTCAGCAGTAGGAGTAAAACTTAAAAACCTGTGTATAAACAACAGGAAATCTTAA

  30   1080      1090      1100      1110      1120      1130      1140
AGAAAATAAAAGGTATCCTTGCAAAGGTTAGTGACCAAACTACTTTTGCGTTTTTCTGTTTTCAGTTTTTTTT

       1150      1160      1170      1180      1190      1200      1210      1220
CTTTCCTTTCCTTATTTTTTTTTCCTTGGAAATCCATCCTTTTAATTAAATAAAACCATTCTTTAAAAATCACT

       1230
TCCAAGTGTT
```

7. US-09-674-593-1' (1-1382)
   US-09-674-593-8 Sequence 8, Application US/09674593

Sequence 8, Application US/09674593
GENERAL INFORMATION:
APPLICANT: Van den Eynde, Benoit
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: TUMOR ASSOCIATED ANTIGEN ENCODED BY THE REVERSE STRAND
TITLE OF INVENTION: OF A NEW UBIQUITOUSLY EXPRESSED GENE
FILE REFERENCE: L0461/7099
CURRENT APPLICATION NUMBER: US/09/674,593
CURRENT FILING DATE: 2000-06-07
PRIOR APPLICATION NUMBER: PCT/US99/10424
PRIOR FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: US 60/085,318
PRIOR FILING DATE: 1998-05-13
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Window Version 3.0
SEQ ID NO 8
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens

Initial Score	=	9	Optimized Score	=	14	Significance	=	-0.44
Residue Identity	=	60%	Matches	=	17	Mismatches	=	8
Gaps	=	3	Conservative Substitutions	=	0			

```
        10        20        30        40        50        60        70
CCAGGAACTTAATTGCTTAATTGGGAGGAGAGAGGTTGAGGTGCAAGAGAGAGAGAAAAG

        80        90       100       110       120       130       140
AAAAATTAGGCTGTTTGGAAAGGGTAGCACACAGATATGATGAGTGTAAGAAAATTGGGTTTCACCATATTTGTGTGTG

       150       160       170       180       190       200       210
TGTGTGTGTGTGGCGTCGCTCCTTCCTCTCTGCCCTCTCCACTAGGCGGTTGAAAGGCCCCGGCGGTTCCCGG

       220       230       240       250       260       270       280
CTCCTGCTCTCAGAAGCTGTCCACCTTGATTCTGCCCCGTAGCAGTGAACCTGGTGTGGTTGGTGCGGCCACTGCGGG

       290       300       310       320       330       340       350
TCCTGAATTGGCTGCCTAGGTGTCACGCCACAGGGTTAATTGACGTCTCACTCCGAGTCCTGCAAGTGCTTGTGTCT

       370       380       390       400       410       420       430
CCCTCTGGGGTGGACGCCCTAGGGCACGGCGGTTACTTCTTCACCTGTGGATTCGTTCGCAGTTTCTGCGTTCGT

       440       450       460       470       480       490       500
TTCAGGAGGCGGATCCGCCCTCGGGTCGGGGTGAGGCCGCTGGGACACGCGGAGGTGCTCTCCCGACGCGCGAAGC
```

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8. US-09-674-593-1' (1-1382)
   US-09-674-593-7 Sequence 7, Application US/09674593

```
        510       520       530       540       550       560       570
AGCGAGCTGAGCGCGGCGGCCAGCGGGGAAGAGTGAGGCGGCGGCCAGCGGCGGCCAGCCGTGTCTCAGCCC
                       x                 x

        580       590       600       610       620       630       640
GTCGTGAAGAGGTGCGTTGTGTTGTGTTACCGGCAAGACGGGACCCCTTCTTACGCGGGGGGGCGCGGGGTCGTGCATGAG

        650       660       670       680       690       700       710
AAGAAGGTGTCCAGCTTCGAAGTCTTCCTGAAGGAGGTGACGGCGGCGGTTCAGGCGCGCACCCTTTGGGGCGTC

        730       740       750       760       770       780       790
AGGAAACATCTACACCCGCGGGACTGGCCACCGAATCCGGAAGAGTCGAGTGTCGGCGAAGCCTAGACGATCCAGAGGTG

        800       810       820       830       840       850       860
GTGGCTGGAGGCCAGGAAGGCCTTCAAGAAACTCAAGTAGTGAGTCGGCTCTCCCCCACCGGCGGGGGCAATTAC

        870       880       890       900       910       920       930
CCCTATAGTGTGGGGTTGGATATGAAGAAATGCAGATCCCTACCCCCCACCACCTCAGTGGTTGAGGGCTGT

       940       950       960       970       980
GACTTCTCGGTGTTGGATTGATGCCCCTCAAAAACTCTCGTTGCAGTTG
```

Sequence 7, Application US/09674593
GENERAL INFORMATION:
APPLICANT: Van den Eynde, Benoit
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: TUMOR ASSOCIATED ANTIGEN ENCODED BY THE REVERSE STRAND
TITLE OF INVENTION: OF A NEW UBIQUITOUSLY EXPRESSED GENE
FILE REFERENCE: L0461/7099
CURRENT APPLICATION NUMBER: US/09/674,593
CURRENT FILING DATE: 2000-06-07
PRIOR APPLICATION NUMBER: PCT/US99/10424
PRIOR FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: US 60/085,318
PRIOR FILING DATE: 1998-05-13
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Window Version 3.0
SEQ ID NO 7
LENGTH: 18
TYPE: DNA
ORGANISM: Homo sapiens

Initial Score	=	7	Optimized Score	=	10	Significance	=	-0.45
Residue Identity	=	57%	Matches	=	12	Mismatches	=	6
Gaps	=	3	Conservative Substitutions	=	0			

```
TAAATG-GGTG-GGC-GGTGGGGGGAGAC
     10              20
     x               x
```

```
        60        70        80        90       100       110       120
AAGGTGCAAGAAGAGAGAGAAAAGAAAAATTAGGCTGTTTGGAAAGGGTAGCACAGATATGATGATGTAAGAAATTG

       130       140       150       160       170       180       190
GGTTTCACCATATTTGTGTGTGTGTGTGTGTGTGGCGTCGCTCCTTCCTCTCTGCCCTCTCACTAGGCGGTGCCTTGTT

       200       210       220       230       240       250       260
TGAAGGCCCCGGCGGTTCCCGGCTCCTGCTCTCAGAAGCTGTCCACCTTGATTCTGCCCGTAGCAGTGAACCT

       270       280       290       300       310       320       330
GGTGTGGTCGGCGCACTGCGGGTCCTGAATTGGCTGCCTAGGTGTCACGCCACAGGGTGAAAAACTTGACGTCTCACTCCGA

       340       350       360       370       380       390       400
GTCCTGCAAGTCCTAGTGTCTCCCTCTGGGTGGGACGCCCTAGGGCACGGCGGTTACTTCTTCTTCACCTGTG

       420       430       440       450       460       470       480
GATTCGTTCAGTTTCTGCGTTCGTTTCAGGAGGCGGATCCGCCCTCGGGTCGGGGTGAGGCCGCTGGGACAGCG

       490       500       510       520       530       540       550
GAGGTGCTCTCCCGACGCGCGAAGCACGCAGCGGAAGAGTGAGCGGCGCAGCGGCGAAGAGTGAGCGCGCAG
                                                                      |||
```